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Agronomic performance of wild emmer wheat germplasm (*Triticum turgidum* ssp. *dicoccoides*) grown under irrigated and rainfed conditions

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Abstract

Background The genetic variations present in wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*), are valuable for improving desirable traits in modern wheat. This research was conducted to evaluate the responses of 105 wild emmer wheat accessions under irrigated and rainfed conditions across two cropping seasons (2021–2022 and 2022–2023) in the field. The following traits were measured: plant height, spike length, number of grains per spike, thousand grain weight, peduncle length, length, days to heading, days to anthesis, days to physiological maturity, soil plant development, protein content, iron content, and zinc content.

Results The combined analysis of variance revealed that the effects of environment and accession type were significant ($p < 0.01$) for all studied agronomic traits. The genotype × environment interaction was also significant ($p < 0.01$) for plant height, number of grains per spike, peduncle length, awn length, days to heading, and days to physiological maturity. Cluster analysis divided the studied accessions into three distinct clusters, revealing that those accessions from different geographical origins were intermixed within each group. Correlation analysis revealed a positive and significant relationship between spike length and the number of grains per spike, as well as between grain iron content and zinc content across all four environments. Multiple scoring index analysis indicated that under irrigated conditions in both years, accessions 68 (DIC291) and 70 (DIC316) were the top performers, whereas under rainfed conditions, accession 56 (DIC256) ranked highest across both years. Accessions that yield well under rainfed conditions are considered highly valuable genetic resources, as they present favorable drought stress resilience traits that increase their adaptability to water-deficit environments.

Conclusions The results showed that the significant genetic diversity observed in wild emmer wheat germplasm under varying conditions highlights its potential for enhancing drought tolerance and improving key agronomic traits, thereby providing valuable resources for breeding programs aimed at increasing the resilience and nutritional quality of bread and durum wheat in water-limited environments.

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Keywords Drought tolerance, Genetic diversity, Grain quality, Phenological traits, Water stress

Background

Wild emmer wheat (*Triticum dicoccoides* BBAA) grows naturally in the Fertile Crescent [1]. The B genome is thought to have originated from an unknown species, with *Aegilops speltoides* (SS) being the closest known relative, whereas its direct ancestor that contributed to the A genome is *Triticum urartu* (AA) [2]. Wild emmer is recognized as the direct ancestor of domesticated emmer wheat (T. *dicoccoum*), durum wheat (*T. durum*), and bread wheat (*T. aestivum*), significantly contributing to the wheat domestication process [3]. The considerable genetic variation present among emmer wheat genotypes in terms of quantitative traits can be leveraged for selection in breeding programs [4]. The high nutritional content and tolerance to various stresses of wild emmer wheat genotypes (*T. dicoccoides*) have made them valuable candidates for use in breeding programs [5, 6].

Wild emmer wheat represents a primary gene pool of cultivated wheat and serves as an invaluable genetic resource for developing new wheat cultivars with improved drought resilience and enhanced nutritional quality [7]. Drought stress triggers several major impairments in plant cells, including dehydration and osmotic stress, loss of cellular turgidity, energy depletion, dysfunction of the plasma and endosomal membranes, metabolic inhibition, chloroplast malfunction, nutritional imbalance, and oxidative stress [8]. Plants employ various strategies to cope with drought, including avoidance, recovery, escape, and tolerance. These mechanisms are more commonly utilized by wild species, making their introgression essential for enhancing crop stress resilience and adaptive plasticity. A shortened duration of phenological stages, such as fewer days to maturity and a shorter grain-filling period, contributes to increased drought tolerance [9]. Therefore, this trait is considered crucial in breeding programs targeting terminal drought stress tolerance. The dietary patterns of a significant portion of the global population are affected by micronutrient deficiencies, especially in essential elements such as iron and zinc. Wheat stands out as a crucial cereal crop, supplying calories to nearly one-third of the global population [5]. Nevertheless, the levels of zinc and iron in wheat are naturally low [10, 11]. Compared with their improved counterparts, wild and ancient wheat tends to contain greater amounts of these micronutrients [5]. The increase in iron and zinc contents in wheat has been achieved through the utilization of wild relatives [11]. Among these, wild emmer wheat (*T. dicoccoides*) serves as a significant genetic resource for improving the quality and micronutrient profile of wheat [10, 12]. Wild emmer wheat is rich in starch, minerals, fiber, carotenoids, and antioxidant compounds, making it a recommended option by healthcare professionals for individuals suffering from allergies, diabetes, and elevated blood cholesterol levels [13, 14]. Furthermore, wild emmer wheat possesses considerable genetic potential to increase the concentrations of zinc, iron, and seed protein, and to improve tolerance to zinc deficiency and drought in cultivated wheat [15]. The protein content of emmer wheat is greater than that of modern wheat, so it has great potential for improving the nutritional value of cultivated wheat [13, 16–18]. This study aimed to assess the genetic diversity of wild emmer wheat in terms of agronomic performance and grain quality traits under both irrigated and rainfed conditions across two growing seasons.

Materials and methods

Plant materials and field trials

In this research, a two-replication alpha lattice design was employed to evaluate 105 wild emmer wheat accessions received from the CREA-GB Genomic and Post-genomic Research Center in Italy (as detailed in Table 1, which is placed at the end of the manuscript) under both irrigated and rainfed conditions during two cropping years. Four distinct environments were designated: E1 for irrigated conditions of the first year (2021–2022), E2 for rainfed conditions of the first year (2021–2022), E3 for irrigated conditions of the second year (2022–2023), and E4 for rainfed conditions of the second year (2022–2023). In both years, each plot contained two rows of 1.5 m in length, with a row spacing of 25 cm and a plant spacing of 6 cm. To ensure appropriate water availability in the irrigated experiments, irrigation was applied at the jointing, booting, heading, and grain filling stages, whereas the rainfed experiments received no supplemental irrigation. To determine the physicochemical characteristics of the soil, composite samples from different parts of the research field were used. The soil characteristics of the experimental site are given in Table 2. The experimental farm is situated at a geographic coordinate of 47 degrees 10 min east longitude and 34 degrees 32 min north latitude, with an elevation of 1350 m above sea level. During the cropping years of 2021–2022, the total rainfall recorded was 285.7 mm, whereas during the cropping years 2022–2023, it was 342.8 mm (Fig. 1).

The following traits were measured: phenological traits, i.e., days to heading, days to anthesis, and days to physiological maturity; and morphological traits, i.e., plant height (cm), awn length (cm), peduncle length (cm), spike length (cm), number of grains per spike and thousand grain weight (g). Ten spikes were randomly selected from each plant for measuring morphological traits.

The thousand grain weight was calculated by sampling 250 grains. In addition, soil plant analysis development (SPAD) as a physiological trait measurement was conducted at the anthesis stage to assess plant senescence in each plot. The chemical composition traits of the grains included soluble grain protein content, which was determined via Bradford's method [19], whereas the concentrations of iron and zinc in the grains were quantified via an atomic absorption spectrometer (Varian 220). The thousand grain weight, grain protein content, and levels of iron and zinc in the grains were measured in one replicate across each environment over a span of two years.

Statistical analyses

The data were subjected to combined analysis of variance (ANOVA) via the GLM procedure of the SAS statistical package, considering the environment as random and the accession number as fixed effects. Pearson phenotypic correlation coefficients were calculated via SPSS IBM 23 software, genetic correlation analysis and principal component analysis were performed via META-R software [20], and cluster analysis via the complete linkage (CLINK) method was carried out via R software [21]. Cluster analysis was conducted using BLUPs (best linear unbiased predictors) for the measured traits across the four environments. BLUPs were calculated across experiments with META-R software using the alpha lattice model (Eq. 1) [20]:

$$\begin{aligned} Yijkl =& \mu + \text{Loc } i + \text{Rep } j \ \ (\text{Loc}) \\ &+ \text{Block } k \ \ (\text{Loc } i\text{Rep}) \\ &+ \text{Gen } l + \text{Loc } l \times \text{Gen } l \\ &+ \varepsilon ijk \end{aligned} \tag{1}$$

where.

μ = Mean effect of the total trait.

Loc *i* = Effect of the ith environment.

Rep *j* (Loc) = Effect of jth replication in the ith environment.

Block *k* (Loc *i*Rep) = Effect of incomplete block *k* in the ith environment in the jth replication.

Gen *l* = Accession lth.

εijk = Residual random effect related to replication, incomplete block, accession and environment.

A multiple scoring index (MSI) based on the measured traits was used to examine the accessions [22]. MSI was calculated via the following (Eq. 2):

$$\text{MSI} = \frac{(X1s + X2s + ...Xns)}{n} \tag{2}$$

where X1s, X2s, and Xns are the scoring scales of each trait when n traits are measured.

Results

Combined analysis of variance and mean comparisons

The results of the combined analysis of variance conducted for the examined traits indicated that both the accessions and the environmental factors had a significant effect on all the measured traits ($P < 0.01$). Additionally, the interaction effect between environment and accession was found to be significant, except for SPAD, spike length, and days to anthesis. The coefficient of variation ranged from 1.97 to 28.84, with the highest values associated with spike length (28.84%), peduncle length (22.95%), and awn length (12.50%) (Table 3).

Descriptive statistics

The interaction effect between environment and accession type was not significant for SPAD, SL, and DTA, allowing for comparisons of these traits across different environments. As shown in Table 4, the highest means for SPAD were observed under irrigation conditions (E3 followed by E1), while lower values were recorded under drought stress conditions (E2 and E4). Spike length was greatest in the E1 and E3 environments, whereas it decreased under drought stress in the E2 and E4 environments. The average days to anthesis were greatest under rainfed conditions (E4), followed by those under irrigation conditions (E3 environment), both in the second year of the experiment. According to Table 4, the heritabilities of the SPAD, PH, NGPS, PL and AL traits were greater in the E1 environment than in the other environments. The highest heritabilities of the SL, DTA and DTPM traits were related to the E2, E3, and E4 environments, respectively. In the case of the DTH trait, the highest heritability was related to the E1 and E3 environments. The findings indicated that SPAD, plant height, spike length, number of grains per spike, and days to physiological maturity were more pronounced under irrigated conditions than under drought conditions (Table 4).

Phenotypic correlation

The Pearson correlation coefficients for the evaluated traits in each environment were calculated (Fig. 2). In the E1 environment, peduncle length was negatively and significantly correlated with days to heading and days to anthesis. Days to heading had a positive and significant correlation with days to anthesis and a negative and significant correlation with thousand grain weight. Days to anthesis was negatively and significantly correlated with the thousand grain weight (Fig. 2A). In E2, the number of grains per spike was positively correlated with peduncle length, days to heading and protein percentage and significantly negatively correlated with awn length and iron content. There was a negative and significant correlation between days to physiological maturity and the thousand grain weight (Fig. 2B). In the E3 environment, there was

Table 1 List of the wild emmer wheat accessions in the research

Number	Accessions	GenBank ACCENUMB	GenBank	Alternative (donor) code	Country Origin
1	DIC001	CItr 17,675	USDA	G 3081	Lebanon
2	DIC002	PI 352,322	USDA	Vavilovii	Lebanon
3	DIC003	PI 352,324	USDA	T-1503	Lebanon
4	DIC009	PI 428,017	USDA	G1395	Turkey
5	DIC011	PI 428,023	USDA	G2050	Turkey
6	DIC014	PI 428,028	USDA	G2059	Turkey
7	DIC015	PI 428,029	USDA	G2060	Turkey
8	DIC023	PI 428,046	USDA	G2090	Turkey
9	DIC026	PI 428,051	USDA	G2103	Turkey
10	DIC027	PI 428,054	USDA	G2108	Turkey
11	DIC030	PI 428,058	USDA	G2116	Turkey
12	DIC033	PI 428,063	USDA	G2125	Turkey
13	DIC038	PI 428,075	USDA	G2146	Turkey
14	DIC041	PI 428,083	USDA	G2166	Turkey
15	DIC044	PI 428,089	USDA	G2186	Turkey
16	DIC044_CA	PI 428,089	USDA	G2186	Turkey
17	DIC045	PI 428,091	USDA	G2188	Turkey
18	DIC046	PI 428,092	USDA	G2844	Turkey
19	DIC048	PI 428,094	USDA	G2995	Palestine
20	DIC058	PI 428,105	USDA	G3028	Palestine
21	DIC061	PI 428,112	USDA	G3036	Palestine
22	DIC068	PI 428,129	USDA	G3096	Lebanon
23	DIC071	PI 428,133	USDA	G3100	Lebanon
24	DIC072	PI 428,137	USDA	G3105	Lebanon
25	DIC075	PI 428,141	USDA	G3112	Lebanon
26	DIC076	PI 428,143	USDA	G3132	Lebanon
27	DIC077	PI 466,928	USDA	A + 6	Syria
28	DIC078	PI 466,931	USDA	A + 22	Syria
29	DIC082	PI 466,939	USDA	A + 42	Syria
30	DIC088	PI 466,946	USDA	A + 79	Syria
31	DIC098	PI 466,958	USDA	I + 7	Palestine
32	DIC100	PI 466,960	USDA	I-9	Palestine
33	DIC130	PI 467,000	USDA	J-38	Palestine
34	DIC133	PI 467,003	USDA	J-47	Palestine
35	DIC144	PI 467,015	USDA	H + 23	Palestine
36	DIC155	PI 470,736	USDA	79TK020-099	Turkey
37	DIC166	PI 470,956	USDA	96	Syria
38	DIC172	PI 470,982	USDA	51	Lebanon
39	DIC179	PI 471,035	USDA	1	Palestine
40	DIC182	PI 471,044	USDA	14	Palestine
41	DIC188	PI 479,779	USDA	I-2	Palestine
42	DIC191	PI 479,782	USDA	M-13	Palestine
43	DIC193	PI 487,254	USDA	SY 20,085	Syria
44	DIC195	PI 487,258	USDA	SY 20,101	Syria
45	DIC196	PI 487,259	USDA	SY 20,110	Syria
46	DIC198	PI 487,263	USDA	SY 20,184	Syria
47	DIC199	PI 487,264	USDA	SY 20,198	Syria
48	DIC200	PI 503,310	USDA	G2040	Turkey
49	DIC225	PI 538,646	USDA	G2095	Turkey
50	DIC227	PI 538,648	USDA	G2097	Turkey
51	DIC229	PI 538,652	USDA	G2112	Turkey
52	DIC230	PI 538,653	USDA	G2114	Turkey
53	DIC248	PI 538,676	USDA	G3003	Palestine

Table 1 (continued)

Number	Accessions	GenBank ACCENUMB	GenBank	Alternative (donor) code	Country Origin
54	DIC249	PI 538,677	USDA	G3004	Palestine
55	DIC250	PI 538,679	USDA	G3007	Palestine
56	DIC256	PI 538,685	USDA	G3027	Palestine
57	DIC258	PI 538,687	USDA	G3037	Palestine
58	DIC259	PI 538,688	USDA	G3038	Palestine
59	DIC261	PI 538,690	USDA	G3050	Palestine
60	DIC263	PI 538,692	USDA	G3052	Palestine
61	DIC264	PI 538,693	USDA	G3053	Palestine
62	DIC267	PI 538,696	USDA	G3064	Palestine
63	DIC268	PI 538,697	USDA	G3065	Palestine
64	DIC283	PI 554,580	USDA	84TK089-017	Turkey
65	DIC284	PI 554,581	USDA	84TK109-079	Turkey
66	DIC285	PI 554,582	USDA	84TK110-087	Turkey
67	DIC286	PI 554,583	USDA	84TK132-001	Turkey
68	DIC291	PI 654,317	USDA	TUR-05-BJS-HB-090	Turkey
69	DIC311	TRI 16,631	IPK	-	Palestine
70	DIC316	TRI 18,478	IPK	PI 427,998	Lebanon
71	DIC326	TRI 18,492	IPK	PI 466,926	Palestine
72	DIC333	TRI 18,499	IPK	PI 470,979	Lebanon
73	DIC334	TRI 18,500	IPK	PI 470,988	Palestine
74	DIC335	TRI 18,501	IPK	PI 470,993	Palestine
75	DIC339	TRI 18,505	IPK	PI 487,253	Syria
76	DIC340	TRI 18,506	IPK	PI487255	Syria
77	DIC342	TRI 18,508	IPK	PI 487,262	Syria
78	DIC346	TRI 18,523	IPK	PI 538,669	Palestine
79	DIC348	TRI 18,528	IPK	PI 538,700	Lebanon
80	DIC350	TRI 18,530	IPK	PI 538,706	Lebanon
81	DIC351	TRI 18,532	IPK	PI 538,714	Lebanon
82	DIC359	TRI 29,352	IPK	PI 538,706	Lebanon
83	DIC375	Unknown	-	-	-
84	DIC376	Unknown	-	-	-
85	DIC380	Unknown	-	-	-
86	DIC386	Unknown	-	-	-
87	DIC391	Unknown	-	-	-
88	TD022	TD022	CREA		Turkey
89	TD076	TD076	CREA		Turkey
90	TD077	TD077	CREA		Turkey
91	TD078	TD078	CREA		Turkey
92	TD080	TD080	CREA		Turkey
93	TD087	TD087	CREA		Turkey
94	TD088	TD088	CREA		Turkey
95	TD089	TD089	CREA		Turkey
96	TD140	TD140	CREA		Turkey
97	TD134	TD134	CREA		Turkey
98	TD135	TD135	CREA		Turkey
99	TD136	TD136	CREA		Turkey
100	TD137	TD137	CREA		Turkey
101	TD216	TD216	CREA		Turkey
102	TD222	TD222	CREA		Turkey
103	TD225	TD225	CREA		Turkey
104	DIC400	8942	CREA		Iran
105	Zavitan	Zavitan	Distelfeld		Palestine

Table 2 Physic-chemical characteristics of the field soil

Sample	Soil texture	pH	Phosphorus (mg/kg)	Potassium (mg/kg)	Nitrogen (%)	Fe (ppm)	Zn (ppm)
Soils of the experimental site	clay loam	7.65	24.38	514.57	0.11	9.06	0.35

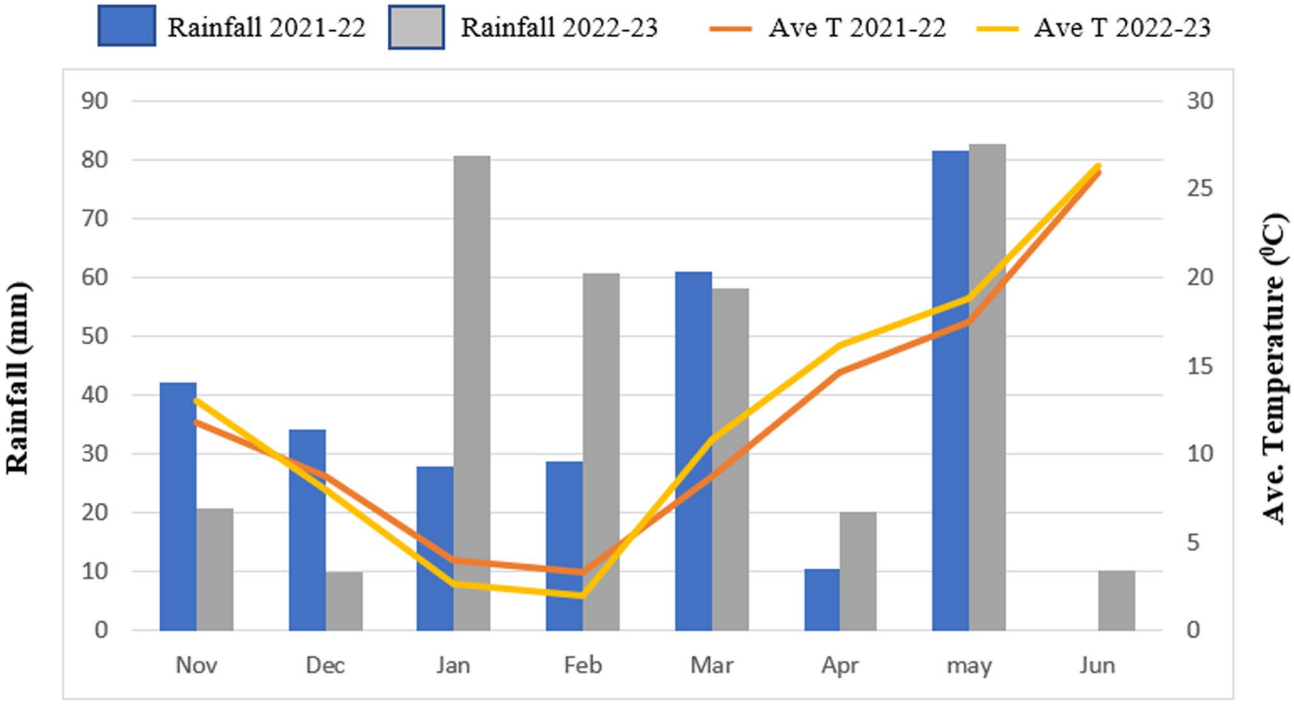


Fig. 1 Temperature and rainfall during two cropping years 2021-22 and 2022-23

Table 3 Combined analysis of variance for the traits studied in 105 wild emmer wheat accessions

Source of variation	df	Mean square								
		SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM
Environment (Env)	3	148.69**	8260.37**	46.49**	200.10**	91.40**	44.72**	5574.34**	1152.96**	508.83**
Replication × Env	4	221.01**	2523.92**	30.06**	110.53**	32.81**	40.65**	336.53**	294.65**	100.90**
Block (Env × Replication)	40	14.63	165.51	9.59	8.96	20.75	1.98	66.78	47.76	59.23
Accession (A)	104	25.05**	1044.45**	17.47**	74.62**	43.71**	12.64**	96.92**	51.04**	84.97**
Env × A	312	9.55^{ns}	157.39**	8.56^{ns}	8.37**	12.28**	3.31**	28.65**	17.20^{ns}	27.70**
Residual	376	12.87	72.74	7.48	3.26	7.74	1.56	19.18	14.83	18.24
CV %	-	6.51	10.40	28.84	10.95	22.95	12.50	2.52	2.12	1.97
LSD 5%	-	4.02	13.61	1.48	2.84	1.55	1.72	4.97	4.65	2.72
Grand mean	-	54.78	82.23	9.48	16.51	12.32	10.01	172.98	181.41	216.36
H^2b	-	0.55	0.86	0.50	0.89	0.74	0.75	0.73	0.62	0.68

The abbreviations used represent: *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity, *CV* Coefficient of variation, *LSD* Least significant difference, H^2b Broad-sense heritability over four environments

a negative and significant correlation between the iron and zinc contents and the thousand-grain weight. Days to anthesis had a positive and significant correlation with days to physiological maturity, and there was a significant negative correlation with zinc content and thousand-grain weight (Fig. 2C). In E4, there was a negative and significant correlation between SPAD values and days to physiological maturity and protein percentage. There was a positive correlation between spike length and the number of grains per spike, peduncle length, days to heading and days to physiological maturity (Fig. 2D).

The findings across all two years indicated that SPAD was positively and significantly correlated with plant height, spike length, and peduncle length under rainfed conditions. Additionally, the results revealed a consistent positive relationship between plant height and spike length, number of grains per spike, and peduncle length across all four conditions. Spike length was positively

Table 4 Descriptive statistics for investigated traits under rainfed and irrigated environments in two cropping seasons

Trait	Irrigated environment 2021-22 (E1)			Rainfed environment 2021-22 (E2)			Irrigated environment 2022-23 (E3)			Rainfed environment 2022-23 (E4)		
	Mean ± S.D.	Range	H^2b	Mean ± S.D.	Range	H^2b	Mean ± S.D.	Range	H^2b	Mean ± S.D.	Range	H^2b
SPAD	55.77 ± 3.29	45.42–64.94	0.12	54.04 ± 4.35	37.19–62.86	0.10	56.17 ± 3.33	45.93–65.41	0.04	54.37 ± 4.48	37.47–67.83	0.07
PH (cm)	86.44 ± 15.74	46.6–121.9.6.9	0.97	74.95 ± 17.49	18.5–121.4.5.4	0.78	89.10 ± 16.88	11.5–123.1.5.1	0.73	77.40 ± 16.97	7.5–122.6.5.6	0.80
SL (cm)	10.31 ± 1.72	6–14.7.7	0.09	9.07 ± 1.70	4.1–16.6	0.77	9.43 ± 2.33	5.2–20.8	0.50	9.10 ± 1.67	5–16	0.56
NGPS	17.94 ± 3.74	11–34.4.4	0.99	15.74 ± 3.79	6.4–32.4	0.88	16.67 ± 4.40	8.1–34.7	0.79	15.62 ± 3.97	6.8–31.4	0.82
PL (cm)	11.25 ± 4.25	4.5–21.8	0.88	11.78 ± 3.52	3.4–22.4	NA	12.88 ± 4.31	5.7–23.2	0.72	12.58 ± 3.52	5.1–23.8	0.21
AL (cm)	9.67 ± 1.92	3.2–15.7	0.99	9.72 ± 1.58	3.4–16.1	0.70	10.72 ± 2.50	4–18.6.6	0.60	9.91 ± 1.79	4–18	0.66
DTH	170.45 ± 8.34	164–187	0.60	166.88 ± 6.03	164–181	0.35	176.67 ± 3.85	168–187	0.60	178.58 ± 5.06	173–189	0.46
DTA	180.47 ± 6.49	170–196	0.43	178.53 ± 4.84	170–187	NA	182.60 ± 4.35	175–195	0.47	184.12 ± 2.92	173–189	0.62
DTPM	217.52 ± 4.65	206–224	0.35	213.94 ± 3.90	209–218	0.59	217.86 ± 6.47	204–229	0.40	215.54 ± 6.99	207–222	0.64

The abbreviations used represent: *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity, *S.D.* Standard deviation, H^2b Broad-sense heritability

correlated with the number of grains per spike in all four conditions. There was a positive correlation between the number of grains per spike and peduncle length in all four conditions and a negative correlation with awn length. Across all four environments, days to heading showed a positive correlation with days to anthesis. A positive relationship was observed between the grain iron and zinc contents under all four conditions.

Genetic correlation

The genetic correlation coefficients for the evaluated traits in each environment were calculated (Tables 5, 6 and 7, and 8). The results showed that under all four conditions, there was a positive and significant genetic correlation between plant height, spike length and the number of grains per spike. The results also revealed a positive and significant genetic correlation between spike length and days to physiological maturity under irrigated conditions. The number of grains per spike under all four conditions had a positive and significant genetic correlation with days to heading. The number of grains per spike under irrigated conditions had a positive and significant genetic correlation with days to anthesis.

Under all four conditions, a significant negative genetic correlation was observed between awn length and days to physiological maturity. Under irrigated conditions, a significant positive genetic correlation was found between days to heading and days to anthesis across both years, with the highest value (0.999**) recorded in both years. In the first year of rainfed conditions (2021–2022), the highest positive and significant genetic correlation was detected between plant height and days to heading (0.708**), whereas the most significant negative correlation was observed between SPAD value and days to physiological maturity (−0.999**). In the second year of rainfed conditions (2022–2023), the strongest positive genetic correlation was noted between plant height and peduncle length (0.935**). while, the greatest negative genetic correlation was found between SPAD and peduncle length (−0.978**).

Principal component analysis

To better understand the relationships between the traits studied in this research, principal component analysis (PCA) was used. Through the PCA method, many variables can be condensed into a few key factors, which effectively summarize the original dataset. As illustrated in Fig. 3, the first two components accounted for 69.39% of the variance in E1, 74.39% in E2, 88.54% in E3, and 83.78% in E4. In E1, the first principal component explained 38.61% of the dataset's variability, demonstrating positive correlations with days to heading, days to anthesis, and awn length but negative correlations with days to physiological maturity, plant height, spike length,

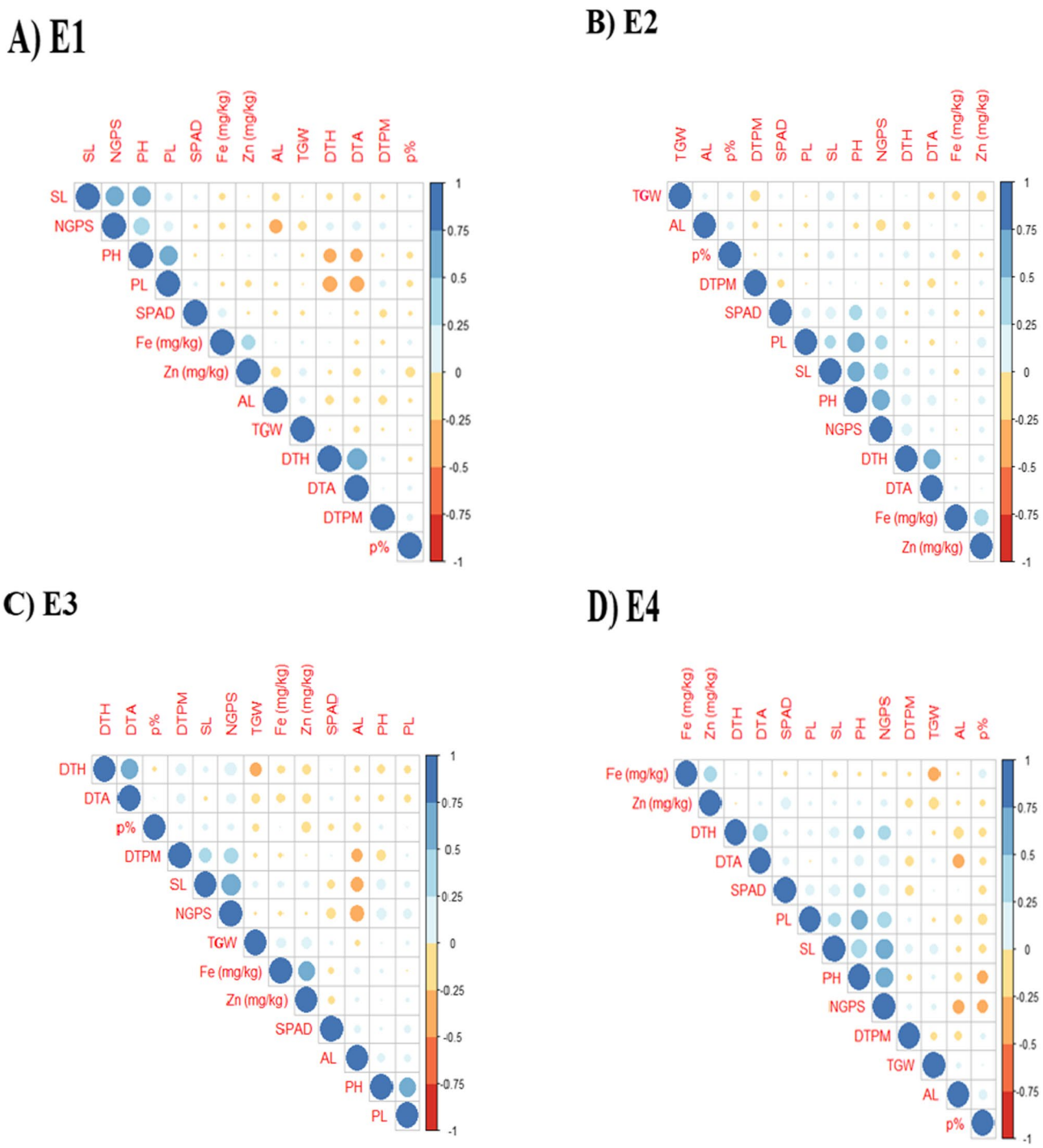


Fig. 2 Phenotypic correlation analysis of the traits studied in the research in two cropping seasons. The abbreviations used represent: (**A**) E1 (irrigated regime 2021–2022), (**B**) E2 (rainfed in 2021–2022), (**C**) E3 (irrigated regime 2022–2023), (**D**) E4 (rainfed in 2022–2023), SPAD: soil plant analysis development, PH: plant height, SL: spike length, NGPS: number of grains per spike, PL: peduncle length, AL: awn length, DTH: days to heading, DTA: days to anthesis, DTPM: days to physiological maturity, P%: Protein percentage, Fe: Iron content, Zn: Zinc content, TGW: thousand grain weight

number of grains per spike, peduncle length, and SPAD. The second principal component in E1 accounted for 30.78% of the variability and was positively associated with peduncle length, awn length, and SPAD but negatively correlated with plant height, spike length, number of grains per spike, days to heading, days to anthesis, and days to physiological maturity (Fig. 3A). In E2, the first principal component explained 45.45% of the dataset's variability and was positively correlated with awn length and SPAD but negatively correlated with plant height,

Table 5 Genetic correlation coefficients of agronomic traits under irrigated conditions in the crop year (2021–2022) (E1)

	SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM
SPAD	1	−0.057^{ns}	−0.714**	−0.143^{ns}	0.086^{ns}	−0.160^{ns}	−0.611**	−0.131^{ns}	0.204**
PH		1	0.639**	0.501**	0.587**	0.019^{ns}	−0.256**	−0.212**	−0.054^{ns}
SL			1	0.391^{ns}	0.282**	−0.543**	−0.512**	0.231**	0.313**
NGPS				1	0.181*	−0.282**	0.212**	0.300**	0.151^{ns}
PL					1	−0.056^{ns}	−0.361**	−0.360**	0.144^{ns}
AL						1	−0.179*	−0.163^{ns}	−0.321**
DTH							1	0.999**	0.010^{ns}
DTA								1	−0.008^{ns}
DTPM									1

The abbreviations used represent: *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity

^{ns}, *, ** non-significant, significant at 5% and 1% level of probability, respectively

Table 6 Genetic correlation coefficients of agronomic traits under rainfed conditions in the crop year (2021–2022) (E2)

	SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM
SPAD	1	0.132^{ns}	0.068^{ns}	−0.038^{ns}	Na	−0.042^{ns}	0.080^{ns}	na	−0.999**
PH		1	0.475**	0.631**	Na	−0.043^{ns}	0.708**	na	−0.086^{ns}
SL			1	0.317**	Na	0.043^{ns}	0.343**	na	0.091^{ns}
NGPS				1	Na	−0.331**	0.431**	na	0.006^{ns}
PL					1	na	na	na	na
AL						1	0.061^{ns}	na	−0.202**
DTH							1	na	0.223**
DTA								1	na
DTPM									1

The abbreviations used represent: *Na* Non-applicable, *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity

^{ns}, *, ** non-significant, significant at 5% and 1% level of probability, respectively

Table 7 Genetic correlation coefficients of agronomic traits under irrigated conditions in the crop year (2022–2023) (E3)

	SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM
SPAD	1	na	na	na	na	na	na	na	na
PH		1	0.608**	0.577**	0.590**	0.073^{ns}	−0.156^{ns}	−0.135^{ns}	−0.006^{ns}
SL			1	0.629**	0.575**	−0.380^{ns}	0.235**	0.105^{ns}	0.265**
NGPS				1	0.493**	−0.435**	0.502**	0.338**	0.456**
PL					1	−0.007^{ns}	−0.093^{ns}	−0.145^{ns}	0.293**
AL						1	−0.194**	0.097^{ns}	−0.539**
DTH							1	0.999**	0.314**
DTA								1	0.139^{ns}
DTPM									1

The abbreviations used represent: *Na* Non-applicable, *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity

^{ns}, *, ** non-significant, significant at 5% and 1% level of probability, respectively

spike length, number of grains per spike, days to heading, and days to physiological maturity. The second principal component in this environment accounted for 28.94% of the variability, showing positive relationships with days to heading and days to physiological maturity but negative correlations with plant height, spike length, number of grains per spike, SPAD, and awn length (Fig. 3B). In E3, the first principal component accounted for 49.68% of the dataset's variability, demonstrating positive correlations with plant height, peduncle length, spike length, the number of grains per spike, and days to physiological maturity but negative correlations with awn length, days to heading, and days to anthesis. The second principal component in this environment explained 38.96% of the dataset's variability, showing positive relationships with spike length, the number of grains per spike, days to heading, days to anthesis, and days to physiological maturity but negative correlations with plant height, peduncle length, and awn length (Fig. 3C). In the fourth environment, the first principal component accounted for 59.73% of the variation in the dataset, was positively influenced by awn length and SPAD, and was negatively

Table 8 Genetic correlation coefficients of agronomic traits under rainfed conditions in the crop year (2022–2023) (E4)

	SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM
SPAD	1	0.503**	−0.175ns	−0.214*	−0.978**	−0.018ns	−0.295**	na	−0.894**
PH		1	0.732**	0.678**	0.935**	−0.150ns	0.411ns	na	−0.080ns
SL			1	0.523**	0.456**	−0.166ns	0.488**	na	0.014ns
NGPS				1	0.787**	−0.396ns	0.603**	na	0.045ns
PL					1	−0.591**	0.228*	na	0.117ns
AL						1	−0.423**	na	−0.267**
DTH							1	na	0.001ns
DTA								1	na
DTPM									1

The abbreviations used represent: *Na* Non-applicable, *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity

ns, *, ** non-significant, significant at 5% and 1% level of probability, respectively

influenced by plant height, spike length, the number of grains per spike, days to heading, peduncle length, and days to physiological maturity. The second principal component in this environment explained 24.05% of the variation in the dataset; it was positively associated with peduncle length and days to physiological maturity but negatively associated with plant height, spike length, the number of grains per spike, awn length, SPAD, and days to heading (Fig. 3D).

Under rainfed conditions in both years, the first principal component was loaded positively by awn length and SPAD and negatively by plant height, spike length, number of grains per spike, days to heading and days to physiological maturity, whereas the second principal component was loaded positively by the days to physiological maturity and negatively by plant height, spike length, number of grains per spike and SPAD.

Cluster analysis

The results of the cluster analysis categorized the examined accessions in the four environments into three distinct groups. The first group (G-I) comprised 72 accessions, the second group (G-II) included 26 accessions, and the third group (G-III) contained 7 accessions (Fig. 4). Each group contained accessions originating from various geographical locations.

Multiple scoring index

Multiple scoring index was used to identify accessions with the best combination of studied traits. Table 9 presents the best accessions exhibiting the optimal combination of traits under the investigated environments. In the irrigated conditions of the first year (E1), the accessions that demonstrated the most advantageous trait combinations were 28, 68, 70, 78, 100, 93, 13, 64, 3, and 82. Conversely, under rainfed conditions in the first year (E2), the accessions that presented the best trait combinations included 105, 20, 69, 57, 103, 8, 89, 45, 96, and 56. In the second year under irrigated conditions (E3), 55, 73, 32, 29, 68, 53, 94, 70, 92, and 89 accessions presented the most favorable combinations of traits. Under the drought conditions of the second year (E4), accessions 71, 47, 56, 50, 18, 79, 94, 88, 97, and 10 presented the best trait combinations. Thus, under irrigated conditions in both years, accessions 68 (DIC291) and 70 (DIC316), and under rainfed conditions in both years, accession number 56 (DIC256) was the best accession studied in terms of the multiple scoring index.

As presented in Table 10, for MSI in the E2 environment, a significant negative correlation was observed exclusively with peduncle length (–0.198*). Additionally, a noteworthy negative correlation was established between plant height and MSI in the E4 environment (–0.210*). No correlations were found between the other environments and the remaining traits.

Discussion

Plant breeding has resulted in genetic erosion as a consequence of the demand for uniformity and the need to increase productivity. To maintain the process of crop improvement and achieve further advancements in resilience to environmental stresses, gradually introducing new genetic variation is essential [23]. Research has been carried out to assess the genetic diversity of wild emmer wheat germplasms originating from various geographical locations, with a focus on agronomic characteristics and certain qualitative traits of the grain. The results of analysis of variance showed significant differences between the accessions studied in the research for all investigated traits. These results are consistent with the research of [24] (wheat) [4], (emmer wheat) [25], (durum wheat) and [14] (emmer wheat). Significant diversity was observed among the wild emmer wheat accessions concerning the traits examined. The high level of genetic variation present in the analyzed germplasm could be effectively utilized in breeding programs for both bread wheat and durum wheat. The interaction effect of environment × accession was significant for plant height, number of grains per spike, peduncle length, awn length, days to heading and days to physiological maturity.

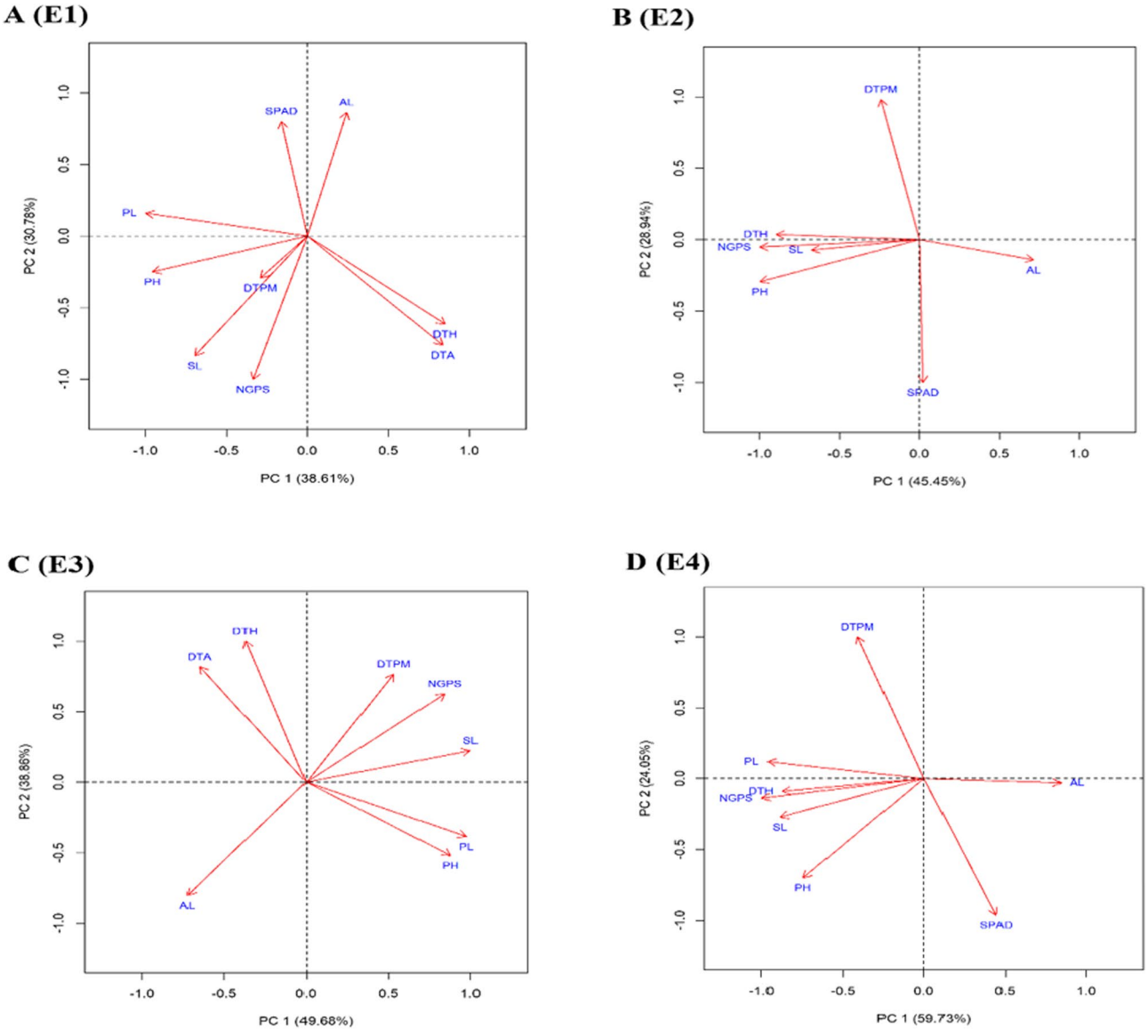


Fig. 3 Principal components analysis of agronomic traits in 105 accessions of wild emmer wheat. The abbreviations used represent: (**A**) irrigated conditions of the first year (2021–2022) (E1), (**B**) rainfed conditions of the first year (2021–2022) (E2), (**C**) irrigated conditions second year (2022–2023) (E3) and (**D**) rainfed conditions of the second year (2022–2023) (E4), SPAD: soil plant analysis development, PH: plant height, SL: spike length, NGPS: number of grains per spike, PL: peduncle length, AL: awn length, DTH: days to heading, DTA: days to anthesis, DTPM: days to physiological maturity

Plant height, spike length, number of grains per spike, peduncle length, days to heading, days to anthesis, and grain iron and zinc contents were positively correlated across all four environments, and these relationships were consistent under both irrigated and rainfed conditions. Additionally, these traits can be modified and improved simultaneously. One study reported a positive and significant correlation between the iron and zinc contents of bread wheat grains under irrigated and rainfed conditions [26]. A thorough investigation is needed to understand the biological or genetic mechanisms that underpin these significant correlations. In terms of the mean performance across the environments, there was a positive and significant correlation between plant height, spike length and peduncle length. Another study reported a positive and significant correlation between plant height and both spike length and peduncle length [27]. A positive and significant correlation was observed between peduncle length and the number of grains per spike. Another study reported a significant and positive correlation between peduncle length and the number of seeds per spike [28]. Previous studies have suggested a highly significant positive correlation between the grain iron and zinc contents in emmer wheat, which is consistent with the results obtained in the present study [10, 29–31]. There was also a positive and significant

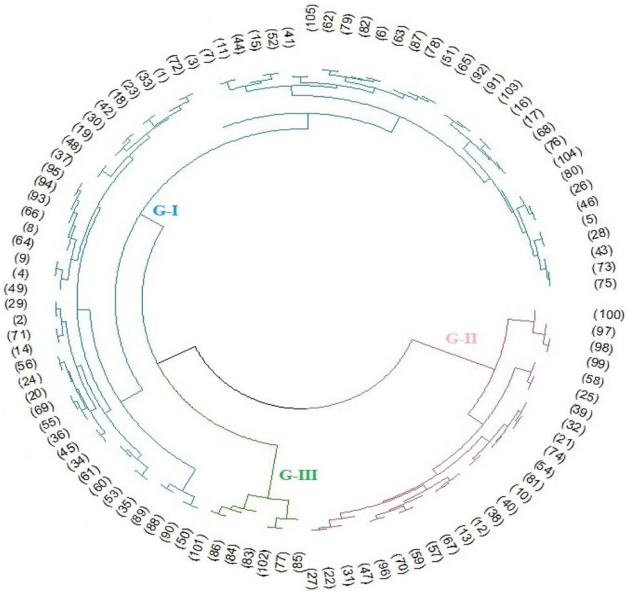


Fig. 4 Cluster analysis of 105 wild emmer wheat accessions using the complete method. Based on the phenotypic data of studied traits shows 3 main clusters (I-III)

correlation between spike length and the number of grains per spike, which was also confirmed by the study of [14] on emmer wheat. Days to heading was strongly and positively associated with days to anthesis. Another study reported positive and significant correlations between days to heading, days to anthesis, and days to physiological maturity [3]. Under irrigated conditions, a negative correlation was observed between spike length and awn length, indicating an inverse relationship between the two traits. Moreover, no relationship was detected between the traits under rainfed conditions and the traits that were affected by both irrigated and rainfed conditions. The results in all four environments revealed that SPAD values were not correlated with plant height, spike length, or peduncle length under irrigated conditions. However, under rainfed conditions, there was a positive correlation between them, indicating that an increase in SPAD corresponds to an increase in plant height, spike length, and peduncle length under rainfed conditions. These results indicate that the relationships among these traits are affected by the irrigated or rainfed conditions of the field. Plant height showed strong positive associations with spike length, grains per spike, and peduncle length. As plant height increased, spike length, the number of grains per spike, and peduncle length tended to increase, whereas a decrease in plant height led to a decrease in these traits. A slight but negative relationship was observed between protein content and the contents of iron (Fe) and zinc (Zn). To understand the relationships between Fe, Zn, and grain protein, it is essential to conduct selection within segregating populations as part of the overall research process. The use of genomic tools will offer additional insights into these associations. The results from the present study also revealed no correlation between the iron content and grain protein content under rainfed conditions; similar results have also been reported in bread wheat [26].

The results of the principal component analysis under rainfed conditions in both years revealed that the first principal component was negatively loaded with days to heading and days to physiological maturity. In one study, the first principal component was loaded positively with the traits of plant height and spike length [3], which was contrary to the results obtained in the present study, which loaded these traits negatively with the first principal component. The results of cluster analysis revealed high genetic diversity in the germplasms used in this study, with different groups containing accessions of different geographical origins. The accessions were mixed with those from various regions and showed no relationship with their geographical origins. These results were also confirmed by [4, 32]. The results of one study revealed a clustering pattern of emmer wheat genotypes with an imbalance between geographical and genetic diversity [4]. They identified genotypes with different geographical origins in different clusters, thus obtaining high genetic diversity in the emmer wheat genotypes studied [4]. A cluster analysis revealed that native and foreign accessions were sporadically present in different groups. They also reported high diversity in accessions [32]. The findings of the multiple scoring index indicate that the ranking of the best accessions varies across different environments, highlighting the significant potential of the wild emmer wheat diversity panel to adapt to varying degrees of drought stress. The accessions that performed well under rainfed conditions are regarded as the most valuable genetic resources, as they possess desirable agronomic traits for adaptation to drought-stressed environments.

Conclusion

Significant variation was observed in the traits of the germplasm of wild emmer wheat under both irrigated and rainfed conditions. Accordingly, genetic variation was observed for both drought escape—indicated by phenological traits such as days to maturity—and drought tolerance, as reflected by agronomic traits such as plant height, number of grains, and grain weight. Across all four environments, significant positive phenotypic and genetic correlations were observed among plant height, spike length, and the number of grains per spike. These findings suggest that under both irrigated and rainfed conditions, increased plant height is associated with increased spike length and number of grains per spike. Furthermore, a positive correlation was observed

Table 9 Multiple scoring index (MSI) with color coding (green = best; red = worst)

Accession number	Accession name	origin	SPAD	PH	SL	NGPS	PL	AL	DTH	DTA	DTPM	MSI
Irrigated environment 2021–22 (E1)												
28	DIC078	Syria	3	7	8	7	10	8	10	6	2	6.7
68	DIC291	Turkey	4	10	10	6	7	8	8	3	6	6.8
70	DIC316	Lebanon	6	6	7	7	8	4	10	9	5	6.8
78	DIC346	Palestine	9	3	8	10	7	8	10	4	3	6.8
100	TD137	Turkey	9	5	2	7	7	8	10	7	7	6.8
93	TD087	Turkey	8	8	8	8	7	9	5	6	4	7.0
13	DIC038	Turkey	8	2	8	9	9	7	3	10	9	7.2
64	DIC283	Turkey	7	8	7	5	5	6	9	10	8	7.2
3	DIC003	Lebanon	9	9	6	8	8	9	2	10	6	7.4
82	DIC359	Lebanon	9	9	10	1	6	10	9	8	9	7.8
Rainfed environment 2021–22 (E2)												
105	Zavitan	Palestine	7	10	7	7	5	6	9	5	3	6.5
20	DIC058	Palestine	10	10	7	4	10	4	6	2	7	6.6
69	DIC311	Palestine	3	4	4	9	9	9	5	8	9	6.6
57	DIC258	Palestine	8	2	8	9	7	5	7	7	8	6.7
103	TD225	Turkey	3	6	9	7	3	8	8	8	10	6.8
8	DIC023	Turkey	5	8	9	2	8	3	10	9	9	7.0
89	TD076	Turkey	5	6	9	10	9	8	5	3	8	7.0
45	DIC196	Syria	10	7	9	6	5	3	9	7	8	7.1
96	TD140	Turkey	4	10	8	8	6	6	9	7	7	7.2
56	DIC256	Palestine	4	10	10	9	6	10	6	7	8	7.7
Irrigated environment 2022–23 (E3)												
55	DIC250	Palestine	5	10	8	2	4	10	9	8	4	6.6
73	DIC334	Palestine	6	7	5	9	7	7	1	10	8	6.6
32	DIC100	Palestine	8	4	7	3	10	10	7	7	5	6.7
29	DIC082	Syria	10	5	5	10	6	9	6	6	5	6.8
68	DIC291	Turkey	7	6	5	8	10	5	6	6	9	6.8
53	DIC248	Palestine	9	6	10	7	6	5	10	8	2	7.0
94	TD088	Turkey	2	9	9	8	7	9	9	7	8	7.5
70	DIC316	Lebanon	10	10	9	3	6	6	8	10	7	7.6
92	TD080	Turkey	7	6	3	10	10	9	9	9	6	7.6
89	TD076	Turkey	10	10	9	3	10	6	10	8	4	7.7
Rainfed environment 2022–23 (E4)												
71	DIC326	Palestine	6	7	7	9	10	5	9	1	4	6.4
47	DIC199	Syria	4	9	10	2	7	2	10	7	8	6.5
56	DIC256	Palestine	6	1	9	4	10	8	5	6	10	6.5
50	DIC227	Turkey	3	7	4	4	5	10	8	10	9	6.6
18	DIC046	Turkey	8	10	5	1	7	10	5	8	7	6.7
79	DIC348	Lebanon	1	9	6	7	8	3	10	9	8	6.7
94	TD088	Turkey	8	6	9	4	9	6	9	4	6	6.7
88	TD022	Turkey	6	6	8	7	10	1	7	8	9	6.8
97	TD134	Turkey	3	9	7	4	8	10	5	7	10	7.0
10	DIC027	Turkey	8	4	10	10	10	9	1	10	5	7.4

The abbreviations used represent: *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity, *MSI* Multiple scoring index

Table 10 Correlation coefficients between studied traits and multiple scoring index (MSI)

MSI-E4	MSI-E3	MSI-E2	MSI-E1	Traits
-0.030^{ns}	0.071^{ns}	0.009^{ns}	0.169^{ns}	SPAD
-0.210*	-0.046^{ns}	-0.129^{ns}	-0.078^{ns}	PH
-0.063^{ns}	0.042^{ns}	-0.072^{ns}	-0.076^{ns}	SL
-0.044^{ns}	0.034^{ns}	-0.043^{ns}	0.005^{ns}	NGPS
-0.183^{ns}	-0.042^{ns}	-0.198*	-0.076^{ns}	PL
0.032^{ns}	0.090^{ns}	0.135^{ns}	-0.104^{ns}	AL
0.077^{ns}	0.048^{ns}	0.019^{ns}	0.093^{ns}	DTH
0.134^{ns}	0.098^{ns}	-0.045^{ns}	0.067^{ns}	DTA
0.072^{ns}	0.100^{ns}	-0.111^{ns}	0.089^{ns}	DTPM
0.184^{ns}	-0.051^{ns}	1	0.208*	MSI-E2
0.073^{ns}	1	-0.051^{ns}	0.104^{ns}	MSI-E3
1	0.073^{ns}	0.184^{ns}	-0.023^{ns}	MSI-E4

The abbreviations used represent: *SPAD* Soil plant analysis development, *PH* Plant height, *SL* Spike length, *NGPS* Number of grains per spike, *PL* Peduncle length, *AL* Awn length, *DTH* Days to heading, *DTA* Days to anthesis, *DTPM* Days to physiological maturity

^{ns}, * non-significant, significant at 5% level of probability, respectively

between the grain iron and zinc contents, suggesting that simultaneous improvement of both traits is achievable. The wide genetic diversity present in the studied wild emmer wheat germplasm offers valuable resources for enhancing drought tolerance. These accessions can play a vital role in breeding programs aimed at enhancing the resilience of bread wheat and durum wheat under water-limited conditions by contributing adaptive traits such as early maturity, improved grain nutritional quality, and increased yield under drought stress.

Abbreviations

A	Accession
AL	Awn length
ANOVA	Analysis of variance
BLUPs	Best linear unbiased predictors
CLINK	Complete linkage
CV	Coefficient of variation
DTA	Days to anthesis
DTH	Days to heading
DTPM	Days to physiological maturity
E1	Environment 1 (irrigated regime 2021-2022)
E2	Environment 2 (rainfed from 2021-2022)
E3	Environment 3 (irrigated regime 2022-2023)
E4	Environment 4 (rainfed from 2022-2023
Env	Environment
Fe	Iron
H^2b	Broad-sense heritability
IPK	The Leibniz Institute of Plant Genetics and Crop Plant Research
LSD	Least significant difference
MSI	Multiple scoring index
na	Non-applicable
NGPS	Number of grains per spike
ns	Non-significant
P%	Protein percentage
PCA	Principal component analysis
PCoA	Principal coordinat analysis
PH	Plant height
PL	Peduncle length
S.D.	Standard deviation
SL	Spike length
SPAD	Soil plant analysis development
TGW	Thousand grain weight
USDA	United States Department of Agriculture
Zn	Zinc

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Authors' contributions
BA performed the experiments. LZ, KCH and SB verified the analytical methods. BA, LZ, KCH and SB drafted the manuscript and EM, AA and HO revised the manuscript. All authors read and approved the final manuscript.

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Data availability
The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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